Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

What is claimed is:

1-48. (Cancelled)

49. (**Currently Amended**) A peptide consisting of a variant of the formula V, RX₆X₇X₈X₉ (SEQ ID No. 293),

wherein

X₆ is arginine, serine or lysine;

 X_7 is leucine, isoleucine or valine;

X₈ is asparagine, alanine, glycine or isoleucine; and

X₉ is a natural or unnatural amino acid selected from the group consisting of leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, parafluorophenylalanine (pFPhe), metafluorophenylalanine (mFPhe), tryptophan, 1-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), metachlorophenylalanine (mClPhe), biphenylalanine (Bip) and 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic).

50. (**Currently Amended**) A peptide consisting of a variant of formula V, RX₆X₇X₈X₉ (SEQ ID No. 293),

wherein:

 X_6 is arginine, serine or lysine;

 X_7 is leucine, isoleucine or valine;

X₈ is asparagine, alanine, glycine or isoleucine; and

X₉ is a natural or unnatural amino acid selected from the group consisting of leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, parafluorophenylalanine (pFPhe), metafluorophenylalanine (mFPhe), tryptophan, 1-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), metachlorophenylalanine (mClPhe), biphenylalanine (Bip) and 1,2,3,4-tetrahydroisoquinoline-3-carboxylic acid (Tic);

or a variant thereof wherein:

(a) R is unchanged or conservatively substituted by a basic amino acid; and/or

- (b) X_6 is substituted by any amino acid capable of providing at least one site for participating in hydrogen bonding; and/or
 - (c) X_7 is unchanged or conservatively substituted.
- 51. (Withdrawn - Currently Amended) A peptide consisting of a variant of the formula V, $RX_6X_7X_8X_9$ (SEQ ID No. 293),

wherein:

X₆ is arginine, serine or lysine;

 X_7 is leucine, isoleucine or valine;

X₈ is asparagine, alanine, glycine or isoleucine; and

X₉ is a natural or unnatural amino acid selected from the group consisting of leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, parafluorophenylalanine (pFPhe), metafluorophenylalanine (mFPhe), tryptophan, 1-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), metachlorophenylalanine (mClPhe), biphenylalanine (Bip) and 1,2,3,4tetrahydroisoquinoline-3-carboxylic acid (Tic);

- or a variant thereof, wherein:
- (a) R is replaced by either a basic amino acid residue or an uncharged natural or unnatural amino acid residue; and/or
- (b) X₆ is replaced by a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage; and/or
- (c) X₇ is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain; and/or
- (d) X_8 is [[is]] replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain.
- 52. (Withdrawn) The peptide of claim 50, wherein R is conservatively substituted by a basic amino acid.
- 53. (Withdrawn) The peptide of claim 50, wherein X₆ is substituted by any amino acid capable of providing at least one site for participating in hydrogen bonding.

54. (Withdrawn) The peptide of claim 50, wherein X_7 is conservatively substituted.

- 55. (Cancelled)
- 56. (Cancelled)
- 57. (Withdrawn) The peptide of claim 51, wherein R is replaced by a basic residue.
- 58. (Withdrawn) The peptide of claim 57, wherein the basic amino acid residue is lysine.
- 59. (Withdrawn) The peptide of claim 51, wherein R is replaced by an uncharged natural or unnatural amino acid residue selected from the group consisting of citrulline (Cit), homoserine, histidine, norleucine (Nle) and glutamine.
- 60. (Withdrawn) The peptide of claim 51, wherein X_6 is replaced by a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage.
- 61. (Withdrawn) The peptide of claim 60, wherein the natural or unnatural amino acid residue is selected from the group consisting of asparagine, proline, aminoisobutyric acid (Aib) and sarcosine (Sar).
- 62. **(Withdrawn)** The peptide of claim 60, wherein the amino acid residue capable of forming a cyclic linkage is ornithine.
- 63. (Withdrawn) The peptide of claim 51, wherein X_7 is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain.
- 64. (**Withdrawn**) The peptide of claim 63, wherein the natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain is selected from the group consisting of norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).

65. (Withdrawn) The peptide of claim 51, wherein X_8 is replaced with a natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain.

66. (Withdrawn) The peptide of claim 65, wherein the natural or unnatural amino acid residue having a slightly larger aromatic or aliphatic side chain is selected from the group consisting of norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).

67-68. (Cancelled)

- 69. **(Previously Presented)** The peptide as in any of claims 49-51, wherein the N-terminal is acylated.
- 70. (Withdrawn) The peptide of claim 50 or 51, wherein R is substituted by citrulline.
- 71. (Previously Presented) A peptide selected from the group consisting of:

H-	Arg	Arg	Leu	Asn	pFPhe	NH_2	(SEQ ID No. 295)
H-	Arg	Arg	Leu	Asn	mClPhe	NH_2	(SEQ ID No. 296)
H-	Arg	Arg	Leu	Ala	pFPhe	NH_2	(SEQ ID No. 298)
H-	Arg	Arg	Leu	Ala	mClPhe	NH_2	(SEQ ID No. 299)
H-	Arg	Arg	Leu	Gly	pFPhe	NH_2	(SEQ ID No. 301)
H-	Arg	Arg	Leu	Gly	mClPhe	NH_2	(SEQ ID No. 302)
H-	Arg	Arg	Ile	Asn	pFPhe	NH_2	(SEQ ID No. 304)
H-	Arg	Arg	lle	Asn	mClPhe	NH_2	(SEQ ID No. 305)
H-	Arg	Arg	Ile	Ala	pFPhe	NH_2	(SEQ ID No. 307)
H-	Arg	Arg	Ile	Ala	mClPhe	NH_2	(SEQ ID No. 308)
H-	Arg	Arg	Ile	Gly	pFPhe	NH_2	(SEQ ID No. 310)
H-	Arg	Arg	Ile	Gly	mClPhe	NH_2	(SEQ ID No. 311)
H-	Arg	Arg	Val	Asn	pFPhe	NH_2	(SEQ ID No. 313)
H-	Arg	Arg	Val	Asn	mClPhe	NH_2	(SEQ ID No. 314)
H-	Arg	Arg	Val	Ala	pFPhe	NH_2	(SEQ ID No. 316)
H-	Arg	Arg	Val	Ala	mClPhe	NH_2	(SEQ ID No. 317)
H-	Arg	Arg	Val	Gly	pFPhe	NH_2	(SEQ ID No. 319)
H-	Arg	Arg	Val	Gly	mClPhe	NH_2	(SEQ ID No. 320)
H-	Arg	Ser	Leu	Asn	pFPhe	NH_2	(SEQ ID No. 322)

H-	Arg	Ser	Leu	Asn	mClPhe	NH_2	(SEQ ID No. 323)
H-	Arg	Ser	Leu	Ala	pFPhe	NH_2	(SEQ ID No. 325)
H-	Arg	Ser	Leu	Ala	mClPhe	NH_2	(SEQ ID No. 326)
H-	Arg	Ser	Leu	Gly	pFPhe	NH_2	(SEQ ID No. 328)
H-	Arg	Ser	Leu	Gly	mClPhe	NH_2	(SEQ ID No. 329)
H-	Arg	Ser	Ile	Asn	pFPhe	NH_2	(SEQ ID No. 331)
H-	Arg	Ser	Ile	Asn	mClPhe	NH_2	(SEQ ID No. 332)
H-	Arg	Ser	lle	Ala	pFPhe	NH_2	(SEQ ID No. 334)
H-	Arg	Ser	Ile	Ala	mClPhe	NH_2	(SEQ ID No. 335)
H-	Arg	Ser	Ile	Gly	pFPhe	NH_2	(SEQ ID No. 337)
H-	Arg	Ser	Ile	Gly	mClPhe	NH_2	(SEQ ID No. 338)
H-	Arg	Ser	Val	Asn	pFPhe	NH_2	(SEQ ID No. 340)
H-	Arg	Ser	Val	Asn	mClPhe	NH_2	(SEQ ID No. 341)
H-	Arg	Ser	Val	Ala	pFPhe	NH_2	(SEQ ID No. 343)
H-	Arg	Ser	Val	Ala	mClPhe	NH_2	(SEQ ID No. 344)
H-	Arg	Ser	Val	Gly	pFPhe	NH_2	(SEQ ID No. 346)
H-	Arg	Ser	Val	Gly	mClPhe	NH_2	(SEQ ID No. 347)
H-	Arg	Lys	Leu	Asn	pFPhe	NH_2	(SEQ ID No. 349)
H-	Arg	Lys	Leu	Asn	mClPhe	NH_2	(SEQ ID No. 350)
H-	Arg	Lys	Leu	Ala	pFPhe	NH_2	(SEQ ID No. 352)
H-	Arg	Lys	Leu	Ala	mClPhe	NH_2	(SEQ ID No. 353)
H-	Arg	Lys	Leu	Gly	pFPhe	NH_2	(SEQ ID No. 355)
H-	Arg	Lys	Leu	Gly	mClPhe	NH_2	(SEQ ID No. 356)
H-	Arg	Lys	Ile	Asn	pFPhe	NH_2	(SEQ ID No. 358)
H-	Arg	Lys	Ile	Asn	mClPhe	NH_2	(SEQ ID No. 359)
H-	Arg	Lys	lle	Ala	pFPhe	NH_2	(SEQ ID No. 361)
H-	Arg	Lys	Ile	Ala	mClPhe	NH_2	(SEQ ID No. 362)
H-	Arg	Lys	Ile	Gly	pFPhe	NH_2	(SEQ ID No. 364)
H-	Arg	Lys	lle	Gly	mClPhe	NH_2	(SEQ ID No. 365)
H-	Arg	Lys	Val	Asn	pFPhe	NH_2	(SEQ ID No. 367)
H-	Arg	Lys	Val	Asn	mClPhe	NH_2	(SEQ ID No. 368)
H-	Arg	Lys	Val	Ala	pFPhe	NH_2	(SEQ ID No. 370)
H-	Arg	Lys	Val	Ala	mClPhe	NH_2	(SEQ ID No. 371)
H-	Arg	Lys	Val	Gly	pFPhe	NH_2	(SEQ ID No. 373)
H-	Arg	Lys	Val	Gly	mClPhe	NH_2	(SEQ ID No. 374)
H-	Arg	Arg	Leu	Ile	pFPhe	NH_2	(SEQ ID No. 375) and
H-	Cit	Cit	Leu	Пе	pFPhe	NH_2	(SEQ ID No. 376).

72. **(Previously Presented)** The peptide of claim 71, wherein the peptide is selected from the group consisting of:

H- Arg Arg Leu Asn pFPhe NH₂ (SEQ ID No. 295)

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H-
    Arg Arg Leu Asn mClPhe
                                    NH_2
                                             (SEQ ID No. 296)
H-
    Arg Arg Leu Ala pFPhe
                                    NH_2
                                             (SEQ ID No. 298)
    Arg Arg Leu Ala mClPhe
                                             (SEQ ID No. 299)
H-
                                    NH_2
    Arg Arg Leu Gly pFPhe
                                             (SEQ ID No. 301)
H-
                                    NH_2
    Arg Arg Leu Gly mClPhe
                                             (SEQ ID No. 302)
H-
                                    NH_2
H-
    Arg Arg Ile
                  Asn pFPhe
                                    NH_2
                                             (SEQ ID No. 304)
H-
                  Asn mClPhe
                                             (SEQ ID No. 305)
    Arg Arg Ile
                                    NH_2
H-
    Arg Arg Ile
                  Ala pFPhe
                                    NH_2
                                             (SEQ ID No. 307)
H-
    Arg Arg Ile
                  Ala mClPhe
                                    NH_2
                                             (SEQ ID No. 308)
H-
    Arg Lys Leu Asn mClPhe
                                    NH_2
                                             (SEQ ID No. 350)
                                             (SEQ ID No. 352)
H-
    Arg Lys Leu Ala pFPhe
                                    NH_2
H-
    Arg Lys Leu Ala
                       mClPhe
                                             (SEQ ID No. 353)
                                    NH_2
H-
    Arg Lys Leu Gly
                       pFPhe
                                    NH_2
                                             (SEQ ID No. 355)
H-
    Arg Lys
             Пe
                  Asn pFPhe
                                    NH_2
                                             (SEQ ID No. 358) and
    Arg Arg Leu Ile
                       pFPhe
                                             (SEQ ID No. 375).
H-
                                    NH_2
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73. **(Previously Presented)** The peptide of claim 71, wherein the peptide is selected from the group consisting of:

H-	Arg	Arg	Leu	Asn	pFPhe	NH_2	(SEQ ID No. 295)
H-	Arg	Arg	Leu	Asn	mClPhe	NH_2	(SEQ ID No. 296)
H-	Arg	Arg	Leu	Ala	pFPhe	NH_2	(SEQ ID No. 298)
H-	Arg	Arg	Leu	Ala	mClPhe	NH_2	(SEQ ID No. 299)
H-	Arg	Arg	Leu	Gly	pFPhe	NH_2	(SEQ ID No. 301)
H-	Arg	Arg	Leu	Gly	mClPhe	NH_2	(SEQ ID No. 302)
H-	Arg	Arg	Ile	Asn	pFPhe	NH_2	(SEQ ID No. 304)
H-	Arg	Arg	Ile	Asn	mClPhe	NH_2	(SEQ ID No. 305)
H-	Arg	Arg	Ile	Ala	pFPhe	NH_2	(SEQ ID No. 307)
H-	Arg	Arg	Ile	Ala	mClPhe	NH_2	(SEQ ID No. 308)
H-	Arg	Lys	Leu	Asn	mClPhe	NH_2	(SEQ ID No. 350)
H-	Arg	Lys	Leu	Ala	pFPhe	NH_2	(SEQ ID No. 352)
H-	Arg	Lys	Leu	Ala	mClPhe	NH_2	(SEQ ID No. 353)
H-	Arg	Lys	Leu	Gly	pFPhe	NH_2	(SEQ ID No. 355)
H-	Arg	Lys	Ile	Asn	pFPhe	NH_2	(SEQ ID No. 358) and
H-	Arg	Arg	Leu	Ile	pFPhe	NH_2	(SEQ ID No. 375).